

Fig. 1

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Human glycoprotein hormone  $\beta 10$  polypeptide:

MKLAFLFLGPMALLLAGYCCVLGASSC  
NLRTFVGCAREFTFLAKKPGCRGLRITTDACWGRCEWKEPPIEIAHHRVCTYNETKQVTVKLPNCAPGVDPFYTPVAIRCDGACSTATTET

Nucleic acid encoding human glycoprotein hormone  $\beta 10$  polypeptide:

ATGAAGCTGGCATTCCTCTTCCCTTGGCCCCCATGGCCCCCTCCTCTCTGGC  
TGGCTATGGCTGTGTCCTCGGTGCCCTCCAGTGGGAACCTGCGCACCTTTTG  
TGGCTGTGCCGTGAGGGAGTTACTTCTTCCCTGGCCAAGAAGCCAGGCTGC  
AGGGCCCTTCGGATCACACGGATGCCCTGCTGGGGTCGCTGTGAGACCTG  
GGAGAAACCCATTCTGGAAACCCCTATATTGAAGCCCATCATCAGTCT  
GTACCTAACAGAGACCAACAGGTGACTGTCAAGCTGCCCAACTGTGCC  
CCGGAGTCGACCCCTTCTACACCTATCCCGTGGCCATCCGCTGTGACTG  
CGGAGCCTGCTCCACTGCCACCAAGGAGTGTGAGACCATCTGAGGCCGCT  
AGCTGCTCTCTGCAGACCCACCTGTGTGAGCAGCACATGC

GAP OF: HUMAN TSH- $\beta$  CHECK: 4247 FROM: 1 TO: 118

TO: HUMAN  $\beta_{10}$       CHECK: 6611    FROM: 1    TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003

QUALITY:	140	LENGTH:	129
RATIO:	1.321	GAPS:	4
PERCENT SIMILARITY:	47.368	<b>PERCENT IDENTITY:</b>	<b>36.842</b>

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

```
| = IDENTITY
: = 2
. = 1
```

HUMAN TSH- $\beta$  X HUMAN  $\beta$ 10

1 .....FCIPTEYTMHIERRECA YCLTINTTICAGYCMTRDINGKL 40

1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWE..KPI 47

41 FLPKYALSQD.VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGKCN 89

48 LEPPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGCACS 97

90 TDYSDCIHEAIKTN YCTKPQKSYLVGFSV 118

```

98  TATTEC..ETI..... 106

```

Fig. 2B

GAP OF: HUMAN FSH- $\beta$  CHECK: 8841 FROM: 1 TO: 111

TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT: 8 AVERAGE MATCH: 2.912  
LENGTH WEIGHT: 2 AVERAGE MISMATCH: -2.003

QUALITY: 156 LENGTH: 122  
RATIO: 1.472 GAPS: 3  
PERCENT SIMILARITY: 44.211 **PERCENT IDENTITY: 35.789**

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

| = IDENTITY  
: = 2  
. = 1

HUMAN FSH- $\beta$  X HUMAN  $\beta$ 10

```
1 .....NSCELTNITIAIEKEECRFCISINTTWCAGYCYTRDL.VYK 40
      | . | . | | : | | | | | : : .
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

41 DPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTPVATQCHCGKCDS 90
      | : ||: | ||: | | | | | | | | . | | | | .
50 PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTPVAIRCDGACSTA 99

91 STDC.TVRGLGPSYCSFGEMKE 111
      .|:| |:
100 TTECETI..... 106
```

# Fig. 2C

GAP OF: HUMAN LH- $\beta$  CHECK: 5679 FROM: 1 TO: 121

TO: HUMAN  $\beta$ 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:  
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP  
COMPCHECK: 6430

GAP WEIGHT: 8 AVERAGE MATCH: 2.912  
LENGTH WEIGHT: 2 AVERAGE MISMATCH: -2.003

QUALITY: 140 LENGTH: 125  
RATIO: 1.321 GAPS: 3  
PERCENT SIMILARITY: 44.118 **PERCENT IDENTITY: 32.353**

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):

| = IDENTITY  
: = 2  
. = 1

HUMAN LH- $\beta$  X HUMAN  $\beta$ 10

1 .SREPLRPW..CHPINAILAVEKEGCPVCITVNTTICAGYCPTMMR.VLQ 46  
| | | . | . | | : : | | | | : : |  
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWEKPILE 49

47 AVLPPPLPQVVCTYRDVRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRS 96  
| | | : : . : | | | | | . : | | : | | | .  
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGACSTA 99

97 TSDCGGPKDHPLTCDHPQLSGLLFL 121  
| . : |  
100 TTECETI..... 106

[illegible]
$$\begin{array}{lcl} | & = & \text{IDENTITY} \\ : & = & 2 \\ . & = & 1 \end{array}$$

```

1  .SKEPLRP..RCRPINATLAVEKEGCPVCITVNTTICAGYCPMTMR.VLQ 46
   |   ||   |   |   .|||   : : | | | | : :|:
1  ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEKPILE 49

47  GVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRS 96
      ||| : : .: || | ||. | .| ||: | | | .
50  PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGACSTA 99

97  TTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ 145
   ||:|
100 TTECETI..... 106

```

The amino acid sequence of the protein is shown in the figure. The sequence is:

**Fig. 3**

